

SEQUENCE LISTING

<110> MACK, Matthias

<120> Antibody and/or chemokine constructs and their use in immunological disorders

<130> E 2411 EP

<140>

<141>

<160> 34

<170> PatentIn Ver. 2.1

<210> 1

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 1

ggaacaagat ggattatcaa gtgtc

25

<210> 2

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 2

ctgtgtatga aaactaagcc atgtg

25

<210> 3

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

tttaccagat ctcaaaaaga ag

22

<210> 4

<211> 21

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 <400> 4
 ggagaaggac aatgttgtag g 21

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 <400> 5
 gacattcagc tgacccagtc tcca 24

<210> 6
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 <400> 6
 gttttatttc cagcttggtc cc 22

<210> 7
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 <400> 7
 accatgggat ggagctgtgt catgctctt 29

<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer
 <400> 8
 tgaggagacg gtgaccgtgg tcccttggcc ccag 34

<210> 9
 <211> 322

<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(321)

<400> 9
gac att cag ctg acc cag tct cca gcc tcc cta tct gca tct gtg gga 48
Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15
gaa act gtc acc atc aca tgt cga gca agt gag aat att tac agt tat 96
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
20 25 30
tta gca tgg tat cag cag aaa cag gga aaa tct cct caa ctc ctg gtc 144
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45
tat aat gca aaa acc tta aca gaa ggt gtg cca tca agg ttc agt ggc 192
Tyr Asn Ala Lys Thr Leu Thr Glu Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
agt gga tca ggc aca cag ttt tct ctg aag atc aac agc ctg cag cct 240
Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80
gaa gat ttt ggg aat tat ttc tgt caa cat cat tat gat act cct cgg 288
Glu Asp Phe Gly Asn Tyr Phe Cys Gln His His Tyr Asp Thr Pro Arg
85 90 95
acg ttc ggt gga ggg acc aag ctg gaa ata aaa c 322
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 10
<211> 107
<212> PRT
<213> Mus sp.

<400> 10
Asp Ile Gln Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
1 5 10 15
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
20 25 30
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
35 40 45
Tyr Asn Ala Lys Thr Leu Thr Glu Gly Val Pro Ser Arg Phe Ser Gly
50 55 60
Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Gly Asn Tyr Phe Cys Gln His His Tyr Asp Thr Pro Arg
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 11
<211> 276
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(276)

<400> 11
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Ala Ser Leu Ser Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg
1 5 10 15
gca agt gag aat att tac agt tat tta gca tgg tat cag cag aaa cag 96
Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln
20 25 30
gga aaa tct cct caa ctc ctg gtc tat aat gca aaa acc tta aca gaa 144
Gly Lys Ser Pro Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Thr Glu
35 40 45
ggt gtg cca tca agg ttc agt ggc agt gga tca ggc aca cag ttt tct 192
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser
50 55 60
ctg aag atc aac agc ctg cag cct gaa gat ttt ggg aat tat ttc tgt 240
Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp Phe Gly Asn Tyr Phe Cys
65 70 75 80
caa cat cat tat gat act cct cgg acg ttc ggt gga 276
Gln His His Tyr Asp Thr Pro Arg Thr Phe Gly Gly
85 90

<210> 12
<211> 92
<212> PRT
<213> Mus sp.

<400> 12
Ala Ser Leu Ser Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Arg
1 5 10 15
Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Gln
20 25 30
Gly Lys Ser Pro Gln Leu Leu Val Tyr Asn Ala Lys Thr Leu Thr Glu

35

40

45

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Gln Phe Ser
 50 55 60

Leu Lys Ile Asn Ser Leu Gln Pro Glu Asp Phe Gly Asn Tyr Phe Cys
 65 70 75 80

Gln His His Tyr Asp Thr Pro Arg Thr Phe Gly Gly
 85 90

<210> 13

<211> 414

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)..(414)

<400> 13

atg gga tgg agc tgt gtc atg ctc ttc ttg gta gca aca gct aca ggt 48
 Met Gly Trp Ser Cys Val Met Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15

gtc cac tcc cag gtc caa ctg cag cag cct ggg gct ggg agg gtg agg 96
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Gly Arg Val Arg
 20 25 30

cct gga gct tca gtg aag ctg tcc tgc aag gct tct ggc tac tcc ttc 144
 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe
 35 40 45

acc agt tac tgg atg aac tgg gtg aag cag agg cct gga caa ggc ctt 192
 Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60

gag tgg att ggc atg att cat cct tcc gat agt gaa act agg tta aat 240
 Glu Trp Ile Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn
 65 70 75 80

cag aag ttc aac gac agg gcc aca ttg act gtt gac aaa tat tcc agc 288
 Gln Lys Phe Asn Asp Arg Ala Thr Leu Thr Val Asp Lys Tyr Ser Ser
 85 90 95

aca gcc tat ata caa ctc agc agc ccg aca tct gag gac tct gcg gtc 336
 Thr Ala Tyr Ile Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val
 100 105 110

tat tac tgt gca aga gga gaa tat tac tac ggt ata ttt gac tac tgg 384
 Tyr Tyr Cys Ala Arg Gly Glu Tyr Tyr Tyr Gly Ile Phe Asp Tyr Trp
 115 120 125

ggc caa ggg acc acg gtc acc gtc tcc tca 414
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser

130

135

<210> 14
 <211> 138
 <212> PRT
 <213> Mus sp.

<400> 14

Met Gly Trp Ser Cys Val Met Leu Phe Leu Val Ala Thr Ala Thr Gly
 1 5 10 15
 Val His Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Gly Arg Val Arg
 20 25 30
 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Ser Phe
 35 40 45
 Thr Ser Tyr Trp Met Asn Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
 50 55 60
 Glu Trp Ile Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn
 65 70 75 80
 Gln Lys Phe Asn Asp Arg Ala Thr Leu Thr Val Asp Lys Tyr Ser Ser
 85 90 95
 Thr Ala Tyr Ile Gln Leu Ser Ser Pro Thr Ser Glu Asp Ser Ala Val
 100 105 110
 Tyr Tyr Cys Ala Arg Gly Glu Tyr Tyr Tyr Gly Ile Phe Asp Tyr Trp
 115 120 125
 Gly Gln Gly Thr Thr Val Thr Val Ser Ser
 130 135

<210> 15
 <211> 354
 <212> DNA
 <213> Mus sp.

<220>

<221> CDS

<222> (2)..(352)

<400> 15

c ttg gta gca aca gct aca ggt gtc cac tcc cag gtc caa ctg cag cag 49
 Leu Val Ala Thr Ala Thr Gly Val His Ser Gln Val Gln Leu Gln Gln
 1 5 10 15
 cct ggg gct ggg agg gtg agg cct gga gct tca gtg aag ctg tcc tgc 97
 Pro Gly Ala Gly Arg Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 20 25 30
 aag gct tct ggc tac tcc ttc acc agt tac tgg atg aac tgg gtg aag 145

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<210> 17

<211> 1545
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (58)..(1545)

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 gat atc gtg ctg acc cag tct cca gcc tcc cta tct gca tct gtg gga 105
 Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly
 1 5 10 15
 gaa act gtc acc atc aca tgt cga gca agt gag aat att tac agt tat 153
 Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr
 20 25 30
 tta gca tgg tat cag cag aaa cag gga aaa tct cct caa ctc ctg gtc 201
 Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val
 35 40 45
 tat aat gca aaa acc tta aca gaa ggt gtg cca tca agg ttc agt ggc 249
 Tyr Asn Ala Lys Thr Leu Thr Glu Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60
 agt gga tca ggc aca cag ttt tct ctg aag atc aac agc ctg cag cct 297
 Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro
 65 70 75 80
 gaa gat ttt ggg aat tat ttc tgt caa cat cat tat gat act cct cgg 345
 Glu Asp Phe Gly Asn Tyr Phe Cys Gln His His Tyr Asp Thr Pro Arg
 85 90 95
 acg ttc ggt gga ggg acc aag ctc gag atc aaa ggt ggt ggt ggt tct 393
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser
 100 105 110
 ggc ggc ggc ggc tcc ggt ggt ggt ggt tct cag gtc caa ctg cag cag 441
 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln
 115 120 125
 cct ggg gct ggg agg gtg agg cct gga gct tca gtg aag ctg tcc tgc 489
 Pro Gly Ala Gly Arg Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys
 130 135 140
 aag gct tct. ggc tac tcc ttc acc agt tac tgg atg aac tgg gtg aag 537
 Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Met Asn Trp Val Lys
 145 150 155 160
 cag agg cct gga caa ggc ctt gag tgg att ggc atg att cat cct tcc 585
 Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Met Ile His Pro Ser
 165 170 175
 gat agt gaa act agg tta aat cag aag ttc aac gac agg gcc aca ttg 633
 Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe Asn Asp Arg Ala Thr Leu

180	185	190	
act gtt gac aaa tat tcc agc aca gcc tat ata caa ctc agc agc ccg Thr Val Asp Lys Tyr Ser Ser Thr Ala Tyr Ile Gln Leu Ser Ser Pro 195 200 205			681
aca tct gag gac tct gcg gtc tat tac tgt gca aga gga gaa tat tac Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Glu Tyr Tyr 210 215 220			729
tac ggt ata ttt gac tac tgg ggc caa ggg acc acg gtc acc gtc tcc Tyr Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser 225 230 235 240			777
tcc gga ggt ggt gga tcc gat atc aaa ctg cag cag tca ggg gct gaa Ser Gly Gly Gly Gly Ser Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu 245 250 255			825
ctg gca aga cct ggg gcc tca gtg aag atg tcc tgc aag act tct ggc Leu Ala Arg Pro Gly Ala Ser Val Lys Met Ser Cys Lys Thr Ser Gly 260 265 270			873
tac acc ttt act agg tac acg atg cac tgg gta aaa cag agg cct gga Tyr Thr Phe Thr Arg Tyr Thr Met His Trp Val Lys Gln Arg Pro Gly 275 280 285			921
cag ggt ctg gaa tgg att gga tac att aat cct agc cgt ggt tat act Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr 290 295 300			969
aat tac aat cag aag ttc aag gac aag gcc aca ttg act aca gac aaa Asn Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys 305 310 315 320			1017
tcc tcc agc aca gcc tac atg caa ctg agc agc ctg aca tct gag gac Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp 325 330 335			1065
tct gca gtc tat tac tgt gca aga tat tat gat gat cat tac tgc ctt Ser Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu 340 345 350			1113
gac tac tgg cgc caa ggc acc act ctc aca gtc tcc tca gtc gaa ggt Asp Tyr Trp Arg Gln Gly Thr Thr Leu Thr Val Ser Ser Val Glu Gly 355 360 365			1161
gga agt gga ggt tct ggt gga agt gga ggt tca ggt gga gtc gac gac Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Val Asp Asp 370 375 380			1209
att cag ctg acc cag tct cca gca atc atg tct gca tct cca ggg gag Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu 385 390 395 400			1257
aag gtc acc atg acc tgc aga gcc agt tca agt gta agt tac atg aac Lys Val Thr Met Thr Cys Arg Ala Ser Ser Val Ser Tyr Met Asn 405 410 415			1305

tgg tac cag cag aag tca ggc acc tcc ccc aaa aga tgg att tat gac	1353
Trp Tyr Gln Gln Lys Ser Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp	
420 425 430	
aca tcc aaa gtg gct tct gga gtc cct tat cgc ttc agt ggc agt ggg	1401
Thr Ser Lys Val Ala Ser Gly Val Pro Tyr Arg Phe Ser Gly Ser Gly	
435 440 445	
tct ggg acc tca tac tct ctc aca atc agc agc atg gag gct gaa gat	1449
Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp	
450 455 460	
gct gcc act tat tac tgc caa cag tgg agt agt aac ccg ctc acg ttc	1497
Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ser Asn Pro Leu Thr Phe	
465 470 475 480	
gga gct ggg acc aag ctg gag ctg aaa cat cat cac cat cat cat tag	1545
Gly Ala Gly Thr Lys Leu Glu Leu Lys His His His His His His	
485 490 495	

<210> 18
 <211> 495
 <212> PRT
 <213> Mus sp.

<400> 18

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ser Ala Ser Val Gly	
1 5 10 15	
Glu Thr Val Thr Ile Thr Cys Arg Ala Ser Glu Asn Ile Tyr Ser Tyr	
20 25 30	
Leu Ala Trp Tyr Gln Gln Lys Gln Gly Lys Ser Pro Gln Leu Leu Val	
35 40 45	
Tyr Asn Ala Lys Thr Leu Thr Glu Gly Val Pro Ser Arg Phe Ser Gly	
50 55 60	
Ser Gly Ser Gly Thr Gln Phe Ser Leu Lys Ile Asn Ser Leu Gln Pro	
65 70 75 80	
Glu Asp Phe Gly Asn Tyr Phe Cys Gln His His Tyr Asp Thr Pro Arg	
85 90 95	
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser	
100 105 110	
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Gln Gln	
115 120 125	
Pro Gly Ala Gly Arg Val Arg Pro Gly Ala Ser Val Lys Leu Ser Cys	
130 135 140	
Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr Trp Met Asn Trp Val Lys	
145 150 155 160	
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Met Ile His Pro Ser	
165 170 175	
Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe Asn Asp Arg Ala Thr Leu	
180 185 190	
Thr Val Asp Lys Tyr Ser Ser Thr Ala Tyr Ile Gln Leu Ser Ser Pro	
195 200 205	
Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys Ala Arg Gly Glu Tyr Tyr	
210 215 220	
Tyr Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser	

225		230		235		240
Ser Gly Gly Gly Gly	Ser Asp Ile Lys	Leu Gln Gln Ser Gly	Ala Glu			
	245	250	255			
Leu Ala Arg Pro Gly	Ala Ser Val Lys	Met Ser Cys Lys	Thr Ser Gly			
	260	265	270			
Tyr Thr Phe Thr Arg	Tyr Thr Met His	Trp Val Lys	Gln Arg Pro Gly			
	275	280	285			
Gln Gly Leu Glu Trp	Ile Gly Tyr Ile	Asn Pro Ser Arg	Gly Tyr Thr			
	290	295	300			
Asn Tyr Asn Gln Lys	Phe Lys Asp Lys	Ala Thr Leu Thr	Thr Asp Lys			
305	310	315	320			
Ser Ser Ser Thr	Ala Tyr Met Gln	Leu Ser Ser	Leu Thr Ser	Glu Asp		
	325	330	335			
Ser Ala Val Tyr	Cys Ala Arg Tyr	Tyr Asp Asp	His Tyr Cys	Leu		
	340	345	350			
Asp Tyr Trp Arg	Gln Gly Thr Thr	Leu Thr Val	Ser Ser Val	Glu Gly		
	355	360	365			
Gly Ser Gly Gly	Ser Gly Gly Ser	Gly Gly Ser	Gly Gly Val	Asp Asp		
	370	375	380			
Ile Gln Leu Thr	Gln Ser Pro Ala	Ile Met Ser	Ala Ser Pro	Gly Glu		
385	390	395	400			
Lys Val Thr Met	Thr Cys Arg Ala	Ser Ser Ser	Val Ser Tyr	Met Asn		
	405	410	415			
Trp Tyr Gln Gln	Lys Ser Gly Thr	Ser Pro Lys	Arg Trp Ile	Tyr Asp		
	420	425	430			
Thr Ser Lys Val	Ala Ser Gly Val	Pro Tyr Arg	Phe Ser Gly	Ser Gly		
	435	440	445			
Ser Gly Thr Ser	Tyr Ser Leu Thr	Ile Ser Ser	Met Glu Ala	Glu Asp		
	450	455	460			
Ala Ala Thr Tyr	Tyr Cys Gln Gln	Trp Ser Ser	Asn Pro Leu	Thr Phe		
465	470	475	480			
Gly Ala Gly Thr	Lys Leu Glu Leu	Lys His His	His His His	His		
	485	490	495			

<210> 19
 <211> 24
 <212> DNA
 <213> Mus sp.

<400> 19
 aaaggcctcc ccatattcct cgga

24

<210> 20
 <211> 37
 <212> DNA
 <213> Mus sp.

<400> 20
 aaagtcgact ccggacatct ccaaagagtt gatgtac

37

<210> 21
 <211> 25
 <212> DNA

<213> Mus sp.

<400> 21

aatccggagg cggcagcctg gccgc

25

<210> 22

<211> 46

<212> DNA

<213> Mus sp.

<400> 22

gggaagctta gtgatggtga tggatgatgct tcaggctctc gcgcgg

46

<210> 23

<211> 1245

<212> DNA

<213> Mus sp.

<220>

<221> CDS

<222> (1)..(1245)

<400> 23

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Ser Pro Tyr Ser Ser Asp Thr Thr Pro Cys Cys Phe Ala Tyr Ile Ala
1 5 10 15

cgc cca ctg ccc cgt gcc cac atc aag gag tat ttc tac acc agt ggc 96
Arg Pro Leu Pro Arg Ala His Ile Lys Glu Tyr Phe Tyr Thr Ser Gly
20 25 30

aag tgc tcc aac cca gca gtc gtc ttt gtc acc cga aag aac cgc caa 144
Lys Cys Ser Asn Pro Ala Val Val Phe Val Thr Arg Lys Asn Arg Gln
35 40 45

gtg tgt gcc aac cca gag aag aaa tgg gtt cgg gag tac atc aac tct 192
Val Cys Ala Asn Pro Glu Lys Lys Trp Val Arg Glu Tyr Ile Asn Ser
50 55 60

ttg gag atg tcc gga ggc ggc agc ctg gcc gcg ctg acc gcg cac cag 240
Leu Glu Met Ser Gly Gly Gly Ser Leu Ala Ala Leu Thr Ala His Gln
65 70 75 80

gct tgc cac ctg ccg ctg gag act ttc acc cgt cat cgc cag ccg cgc 288
Ala Cys His Leu Pro Leu Glu Thr Phe Thr Arg His Arg Gln Pro Arg
85 90 95

ggc tgg gaa caa ctg gag cag tgc ggc tat ccg gtg cag cgg ctg gtc 336
Gly Trp Glu Gln Leu Glu Gln Cys Gly Tyr Pro Val Gln Arg Leu Val
100 105 110

gcc ctc tac ctg gcg gcg cgg ctg tcg tgg aac cag gtc gac cag gtg 384
Ala Leu Tyr Leu Ala Ala Arg Leu Ser Trp Asn Gln Val Asp Gln Val
115 120 125

atc cgc aac gcc ctg gcc agc ccc ggc agc ggc ggc gac ctg ggc gaa	432
Ile Arg Asn Ala Leu Ala Ser Pro Gly Ser Gly Gly Asp Leu Gly Glu	
130 135 140	
gcg atc cgc gag cag ccg gag cag gcc cgt ctg gcc ctg acc ctg gcc	480
Ala Ile Arg Glu Gln Pro Glu Gln Ala Arg Leu Ala Leu Thr Leu Ala	
145 150 155 160	
gcc gcc gag agc gag cgc ttc gtc cgg cag ggc acc ggc aac gac gag	528
Ala Ala Glu Ser Glu Arg Phe Val Arg Gln Gly Thr Gly Asn Asp Glu	
165 170 175	
gcc ggc gcg gcc aac ggc ccg gcg gac agc ggc gac gcc ctg ctg gag	576
Ala Gly Ala Ala Asn Gly Pro Ala Asp Ser Gly Asp Ala Leu Leu Glu	
180 185 190	
cgc aac tat ccc act ggc gcg gag ttc ctc ggc gac ggc ggc gac gtc	624
Arg Asn Tyr Pro Thr Gly Ala Glu Phe Leu Gly Asp Gly Gly Asp Val	
195 200 205	
agc ttc agc acc cgc ggc acg cag aac tgg acg gtg gag cgg ctg ctc	672
Ser Phe Ser Thr Arg Gly Thr Gln Asn Trp Thr Val Glu Arg Leu Leu	
210 215 220	
cag gcg cac cgc caa ctg gag gag cgc ggc tat gtg ttc gtc ggc tac	720
Gln Ala His Arg Gln Leu Glu Glu Arg Gly Tyr Val Phe Val Gly Tyr	
225 230 235 240	
cac ggc acc ttc ctc gaa gcg gcg caa agc atc gtc ttc ggc ggg gtg	768
His Gly Thr Phe Leu Glu Ala Ala Gln Ser Ile Val Phe Gly Gly Val	
245 250 255	
cgc gcg cgc agc cag gac ctc gac gcg atc tgg cgc ggt ttc tat atc	816
Arg Ala Arg Ser Gln Asp Leu Asp Ala Ile Trp Arg Gly Phe Tyr Ile	
260 265 270	
gcc ggc gat ccg gcg ctg gcc tac ggc tac gcc cag gac cag gaa ccc	864
Ala Gly Asp Pro Ala Leu Ala Tyr Gly Tyr Ala Gln Asp Gln Glu Pro	
275 280 285	
gac gca cgc ggc cgg atc cgc aac ggt gcc ctg ctg cgg gtc tat gtg	912
Asp Ala Arg Gly Arg Ile Arg Asn Gly Ala Leu Leu Arg Val Tyr Val	
290 295 300	
ccg cgc tcg agc ctg ccg ggc ttc tac cgc acc agc ctg acc ctg gcc	960
Pro Arg Ser Ser Leu Pro Gly Phe Tyr Arg Thr Ser Leu Thr Leu Ala	
305 310 315 320	
gcg ccg gag gcg gcg ggc gag gtc gaa cgg ctg atc ggc cat ccg ctg	1008
Ala Pro Glu Ala Ala Gly Glu Val Glu Arg Leu Ile Gly His Pro Leu	
325 330 335	
ccg ctg cgc ctg gac gcc atc acc ggc ccc gag gag gaa ggc ggg cgc	1056
Pro Leu Arg Leu Asp Ala Ile Thr Gly Pro Glu Glu Glu Gly Gly Arg	
340 345 350	
ctg gag acc att ctc ggc tgg ccg ctg gcc gag cgc acc gtg gtg att	1104

Leu	Glu	Thr	Ile	Leu	Gly	Trp	Pro	Leu	Ala	Glu	Arg	Thr	Val	Val	Ile		
		355					360					365					
ccc	tcg	gcg	atc	ccc	acc	gac	ccg	cgc	aac	gtc	ggc	ggc	gac	ctc	gac	1152	
Pro	Ser	Ala	Ile	Pro	Thr	Asp	Pro	Arg	Asn	Val	Gly	Gly	Asp	Leu	Asp		
		370				375					380						
ccg	tcc	agc	atc	ccc	gac	aag	gaa	cag	gcg	atc	agc	gcc	ctg	ccg	gac	1200	
Pro	Ser	Ser	Ile	Pro	Asp	Lys	Glu	Gln	Ala	Ile	Ser	Ala	Leu	Pro	Asp		
					390					395					400		
tac	gcc	agc	cag	ccc	ggc	aaa	ccg	ccg	cgc	gag	gac	ctg	aag	taa		1245	
Tyr	Ala	Ser	Gln	Pro	Gly	Lys	Pro	Pro	Arg	Glu	Asp	Leu	Lys				
				405					410					415			

<210> 24
 <211> 414
 <212> PRT
 <213> Mus sp.

<400> 24

Ser	Pro	Tyr	Ser	Ser	Asp	Thr	Thr	Pro	Cys	Cys	Phe	Ala	Tyr	Ile	Ala		
1				5					10					15			
Arg	Pro	Leu	Pro	Arg	Ala	His	Ile	Lys	Glu	Tyr	Phe	Tyr	Thr	Ser	Gly		
			20					25					30				
Lys	Cys	Ser	Asn	Pro	Ala	Val	Val	Phe	Val	Thr	Arg	Lys	Asn	Arg	Gln		
		35					40					45					
Val	Cys	Ala	Asn	Pro	Glu	Lys	Lys	Trp	Val	Arg	Glu	Tyr	Ile	Asn	Ser		
	50					55				60							
Leu	Glu	Met	Ser	Gly	Gly	Gly	Ser	Leu	Ala	Ala	Leu	Thr	Ala	His	Gln		
	65				70					75					80		
Ala	Cys	His	Leu	Pro	Leu	Glu	Thr	Phe	Thr	Arg	His	Arg	Gln	Pro	Arg		
				85					90					95			
Gly	Trp	Glu	Gln	Leu	Glu	Gln	Cys	Gly	Tyr	Pro	Val	Gln	Arg	Leu	Val		
		100						105					110				
Ala	Leu	Tyr	Leu	Ala	Ala	Arg	Leu	Ser	Trp	Asn	Gln	Val	Asp	Gln	Val		
	115					120					125						
Ile	Arg	Asn	Ala	Leu	Ala	Ser	Pro	Gly	Ser	Gly	Gly	Asp	Leu	Gly	Glu		
	130					135					140						
Ala	Ile	Arg	Glu	Gln	Pro	Glu	Gln	Ala	Arg	Leu	Ala	Leu	Thr	Leu	Ala		
	145				150				155						160		
Ala	Ala	Glu	Ser	Glu	Arg	Phe	Val	Arg	Gln	Gly	Thr	Gly	Asn	Asp	Glu		
			165					170						175			
Ala	Gly	Ala	Ala	Asn	Gly	Pro	Ala	Asp	Ser	Gly	Asp	Ala	Leu	Leu	Glu		
		180						185					190				
Arg	Asn	Tyr	Pro	Thr	Gly	Ala	Glu	Phe	Leu	Gly	Asp	Gly	Gly	Asp	Val		
	195					200					205						
Ser	Phe	Ser	Thr	Arg	Gly	Thr	Gln	Asn	Trp	Thr	Val	Glu	Arg	Leu	Leu		
	210					215					220						
Gln	Ala	His	Arg	Gln	Leu	Glu	Glu	Arg	Gly	Tyr	Val	Phe	Val	Gly	Tyr		
	225				230					235					240		
His	Gly	Thr	Phe	Leu	Glu	Ala	Ala	Gln	Ser	Ile	Val	Phe	Gly	Gly	Val		
				245				250						255			
Arg	Ala	Arg	Ser	Gln	Asp	Leu	Asp	Ala	Ile	Trp	Arg	Gly	Phe	Tyr	Ile		
			260					265					270				
Ala	Gly	Asp	Pro	Ala	Leu	Ala	Tyr	Gly	Tyr	Ala	Gln	Asp	Gln	Glu	Pro		

	275		280		285
Asp	Ala Arg Gly Arg Ile	Arg Asn Gly Ala Leu	Leu Arg Val Tyr Val		
290		295	300		
Pro	Arg Ser Ser Leu Pro	Gly Phe Tyr Arg Thr	Ser Leu Thr Leu Ala		
305	310	315	320		
Ala	Pro Glu Ala Ala Gly	Glu Val Glu Arg Leu	Ile Gly His Pro Leu		
	325	330	335		
Pro	Leu Arg Leu Asp Ala	Ile Thr Gly Pro Glu	Glu Glu Gly Gly Arg		
	340	345	350		
Leu	Glu Thr Ile Leu Gly	Trp Pro Leu Ala Glu	Arg Thr Val Val Ile		
	355	360	365		
Pro	Ser Ala Ile Pro Thr	Asp Pro Arg Asn Val	Gly Gly Asp Leu Asp		
	370	375	380		
Pro	Ser Ser Ile Pro Asp	Lys Glu Gln Ala Ile	Ser Ala Leu Pro Asp		
385	390	395	400		
Tyr	Ala Ser Gln Pro Gly	Lys Pro Pro Arg Glu	Asp Leu Lys		
	405	410			

<210> 25
 <211> 363
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(363)

<400> 25	
gat atc aaa ctg cag cag tca ggg gct gaa ctg gca aga cct ggg gcc	48
Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala	
1 5 10 15	
tca gtg aag atg tcc tgc aag act tct ggc tac acc ttt act agg tac	96
Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr	
20 25 30	
acg atg cac tgg gta aaa cag agg cct gga cag ggt ctg gaa tgg att	144
Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile	
35 40 45	
gga tac att aat cct agc cgt ggt tat act aat tac aat cag aag ttc	192
Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe	
50 55 60	
aag gac aag gcc aca ttg act aca gac aaa tcc tcc agc aca gcc tac	240
Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr	
65 70 75 80	
atg caa ctg agc agc ctg aca tct gag gac tct gca gtc tat tac tgt	288
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
85 90 95	
gca aga tat tat gat gat cat tac tgc ctt gac tac tgg cgc caa ggc	336
Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Arg Gln Gly	
100 105 110	

acc act ctc aca gtc tcc tca gtc gaa
 Thr Thr Leu Thr Val Ser Ser Val Glu
 115 120

363

<210> 26
 <211> 121
 <212> PRT
 <213> Mus sp.

<400> 26
 Asp Ile Lys Leu Gln Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly Ala
 1 5 10 15
 Ser Val Lys Met Ser Cys Lys Thr Ser Gly Tyr Thr Phe Thr Arg Tyr
 20 25 30
 Thr Met His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45
 Gly Tyr Ile Asn Pro Ser Arg Gly Tyr Thr Asn Tyr Asn Gln Lys Phe
 50 55 60
 Lys Asp Lys Ala Thr Leu Thr Thr Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
 85 90 95
 Ala Arg Tyr Tyr Asp Asp His Tyr Cys Leu Asp Tyr Trp Arg Gln Gly
 100 105 110
 Thr Thr Leu Thr Val Ser Ser Val Glu
 115 120

<210> 27
 <211> 324
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(324)

<400> 27
 gtc gac gac att cag ctg acc cag tct cca gca atc atg tct gca tct 48
 Val Asp Asp Ile Gln Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser
 1 5 10 15
 cca ggg gag aag gtc acc atg acc tgc aga gcc agt tca agt gta agt 96
 Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser
 20 25 30
 tac atg aac tgg tac cag cag aag tca ggc acc tcc ccc aaa aga tgg 144

Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg	Trp	
		35					40					45				
att	tat	gac	aca	tcc	aaa	gtg	gct	tct	gga	gtc	cct	tat	cgc	ttc	agt	192
Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	Tyr	Arg	Phe	Ser	
	50					55					60					
ggc	agt	ggg	tct	ggg	acc	tca	tac	tct	ctc	aca	atc	agc	agc	atg	gag	240
Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Met	Glu	
	65				70					75					80	
gct	gaa	gat	gct	gcc	act	tat	tac	tgc	caa	cag	tgg	agt	agt	aac	ccg	288
Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	
				85					90					95		
ctc	acg	ttc	gga	gct	ggg	acc	aag	ctg	gag	ctg	aaa					324
Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys					
			100					105								

<210> 28
 <211> 108
 <212> PRT
 <213> Mus sp.

<400> 28																
Val	Asp	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met	Ser	Ala	Ser	
	1			5					10					15		
Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Val	Ser	
			20					25					30			
Tyr	Met	Asn	Trp	Tyr	Gln	Gln	Lys	Ser	Gly	Thr	Ser	Pro	Lys	Arg	Trp	
		35					40					45				
Ile	Tyr	Asp	Thr	Ser	Lys	Val	Ala	Ser	Gly	Val	Pro	Tyr	Arg	Phe	Ser	
	50					55					60					
Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser	Ser	Met	Glu	
	65				70					75					80	
Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Trp	Ser	Ser	Asn	Pro	
				85					90					95		
Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys					
			100					105								

<210> 29
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 29

Arg Ala Ser Glu Asn Ile Tyr Ser Tyr Leu Ala
1 5 10

<210> 30

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 30

Asn Ala Lys Thr Leu Thr Glu
1 5

<210> 31

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 31

Gln His His Tyr Asp Thr Pro Arg Thr
1 5

<210> 32

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 32

Tyr Trp Met Asn
1

<210> 33

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 33

Gly Met Ile His Pro Ser Asp Ser Glu Thr Arg Leu Asn Gln Lys Phe
1 5 10 15

Asn Asp Arg

<210> 34

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 34

Gly	Glu	Tyr	Tyr	Tyr	Gly	Ile	Phe	Asp	Tyr
1				5					10